

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 31, 2003, 13:09:31 ; Search time 83 seconds
(without alignments)
1005.906 Million cell updates/sec

Title: US-10-082-894-2

Perfect score: 2786

Sequence: 1 MDRYQNVQKVCVLWIDWG.....LMGLPVPENDGVPLLEQRG 526

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141.5	41.0	510	23	AB48814
2	996	35.8	491	19	AAW28502
3	992	35.6	505	22	AAW28503
4	992	35.6	517	23	ABP40599
5	736.5	26.4	557	18	AAW28504
6	729	26.2	560	21	AAW28505
7	706	25.3	557	21	AAW28506
8	703	25.2	560	18	AAW28507
9	696	25.0	556	18	AAW28508

10	694	24.9	555	18	AAW28503	Timothy grass poll
11	687	24.7	575	21	AAW28502	Arabidopsis thalia
12	686	24.6	530	18	AAW28501	Birch pollen co-fa
13	657	23.6	511	21	AAW28504	Arabidopsis thalia
14	647	23.2	510	21	AAW28503	Arabidopsis thalia
15	628	22.5	528	21	AAW28503	Arabidopsis thalia
16	612	22.0	482	21	AAW28503	Arabidopsis thalia
17	605	21.7	481	21	AAW28503	Arabidopsis thalia
18	585	21.0	499	21	AAW28503	Arabidopsis thalia
19	568.5	20.4	425	22	AAW28503	Novel human diagno
20	466	16.7	424	21	AAW28503	Arabidopsis thalia
21	425.5	15.3	353	21	AAW28503	Arabidopsis thalia
22	419.5	15.1	349	21	AAW28503	Arabidopsis thalia
23	333	12.0	161	19	AAW28503	Ehrlichia sp. HGE-
24	333	12.0	161	21	AAW28503	Ehrlichia antigen
25	333	12.0	161	23	AAW28503	Ehrlichia antigen
26	333	12.0	161	23	AAW28503	Human granulocytic
27	221	7.9	150	21	AAW28503	Zea mays protein f
28	214	7.7	136	21	AAW28503	Zea mays protein f
29	195	7.0	84	23	AAW28503	Helicobacter pylor
30	179	6.4	128	21	AAW28503	Zea mays protein f
31	179	6.4	166	21	AAW28503	Zea mays protein f
32	164	5.9	98	21	AAW28503	Zea mays protein f
33	160.5	5.8	74	23	AAW28503	Human ORFX protein
34	159.5	5.7	61	23	AAW28503	Human ORF2746 prot
35	156	5.6	102	21	AAW28503	Zea mays protein f
36	154	5.5	107	21	AAW28503	Zea mays protein f
37	149	5.3	91	21	AAW28503	Zea mays protein f
38	147.5	5.3	102	18	AAW28503	Amino acid sequenc
39	121	4.3	413	22	AAW28503	Putative P. abyss
40	114	4.1	83	21	AAW28503	Zea mays protein f
41	110	3.9	431	22	AAW28503	Human gene 5 encod
42	110	3.9	709	22	AAW28503	C. elegans sulfata
43	110	3.9	880	22	AAW28503	Drosophila melanog
44	110	3.9	896	22	AAW28503	Human EST encoded
45	110	3.9	1089	21	AAW28503	Human PRO1249 (UNQ

ALIGNMENTS

RESULT 1

AB48814
ID AB48814 standard; Protein; 510 AA.

XX AC AB48814;

XX DT 05-FEB-2002 (first entry)

XX DE Listeria monocytogenes protein #1518.

XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

XX KW vitamin B12; bacterial infection; disease.

XX OS Listeria monocytogenes.

XX PN WO200177335-A2.

XX PD 18-OCT-2001.

XX PF 11-APR-2001; 2001WO-FR01118.

XX PR 11-APR-2000; 2000FR-0004629.

XX (INSP) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;

XX Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;

XX Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;

XX Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;

XX Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;

XX Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;

XX Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;

PI Rose M, Voss H;
XX WPI; 2002-010914/01.
XX
XX
XX Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
PT and prevention of *Listeria* and related bacterial infections, and
PT related polypeptides
XX
XX
XX Claim 6; SEQ ID No 1519; 192pp; French.
XX
XX
XX The present invention relates to the genome sequence of *Listeria*
CC *monocytogenes* EGB-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in *L.*
CC *monocytogenes* and related organisms, and for studying genetic
CC polymorphisms and related genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of *L. monocytogenes* and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccine compositions for the treatment or prevention of infections by *L.*
CC *monocytogenes* and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 510 AA;

Query Match 41.0%; Score 1141.5; DB 23; Length 510;
Best Local Similarity 44.0%; Pred. No. 3.6e-105;
Matches 230; Conservative 92; Mismatches 174; Indels 27; Gaps 7;

QY 11 VCLVVDGCLSDQHGNAIAKAKTPIMDKLCSGNWQ-----KLEAHGLHVLGPEGLMGN 65
DB 6 VAIILDGFGKRAETVGNVAQANKPNFDY-----WADFFPHGELKAAGLDVGLPEQOMGN 61
QY 66 SEVGHNLNIGAGRVYQDVRINLAVORNEFTNPQIVASAEKKGSRHLHLGLVSDGG 125
DB 62 SEVGHNLNIGAGRVYQDVRINLAVORNEFTNPQIVASAEKKGSRHLHLGLVSDGG 121
QY 126 VHSIDHLFALIRAFKQLOPKVPIHFADGRDTSPTSGAGYLEQLQFIASEKYELAT 185
DB 122 VHSIDHLFALIRAFKQLOPKVPIHFADGRDTSPTSGAGYLEQLQFIASEKYELAT 181
QY 186 ITGRVYAMDGRKWERIKMAYEAIVGIGOKATVDKAVDVVRERYAQSEDFELKPIVFS 245
DB 182 VSGRFYAMDGRKWERIKMAYEAIVGIGOKATVDKAVDVVRERYAQSEDFELKPIVFS 239
QY 246 DGRG----VKDDDTLFFNRYADRMQICECLGLERYKDLNLSVPHKNIQISGMTYNNK 301
DB 240 KDGKPVATKNDNAVIFNRPDRALQLSNATDKWDHFDRCADHPKNIKFTWTLYNP 299
QY 302 EPPFPFLPPVTHNNVLAEWLASQGVTFQHCATEKYPHVTFFNGREVFQDERCMY 361
DB 300 SIDAFAEPPIEMKNVIGEVLSNEGLSQLRAIEATEKYPHVTFFNGREVFQDERCMY 359
QY 362 PSPKEVATYDLKPEMNAAGVAEKVQIESGRHPLVCMFAPDPDWGHTGKPEPAVCAQ 421
DB 360 NSPK-VETVYDLPENSAYEVTALVEDIKNDHAILNFAFNDPVGVHSGMLEPTIKATE 418
QY 422 ATDEATGKFEACQTYNNVLTSDHGNAEKMIAPDGSHTAHTCNLVPFTCSSFTFVK 481
DB 419 AVDENLGRVVDLLEKGSAILFADHGNSETSTEGKPHTAHTVPPVPIVTK----- 473
QY 482 STPTPTGDDGKERARALRDVAPTVLQMLPVPPEMDGVPLLEQ 524
DB 474 -----GVTLREGGR-LADVAPTMLDLGLVKKPAEMTGESLIQ 510

RESULT 2

AAW98438

ID AAW98438 standard; Protein; 491 AA.
XX
AC AAW98438;
XX
DT 31-MAR-1999 (first entry)
XX
DE H. pylori GHPO 476 protein.
XX
XX GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
KW peptic ulcer disease.
XX
OS Helicobacter pylori.
XX
PN WO9843478-A1.
XX
PD 08-OCT-1998.
XX
XX 01-APR-1998; 98WO-US06371.
XX
PR 29-JUL-1997; 97US-0902615.
XX
PR 01-APR-1997; 97US-0833457.
XX
PR 24-JUN-1997; 97US-0881227.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
XX
XX Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J;
XX
XX WPI; 1998-542293/46.
DR N-PSDB; AAX14157.
XX
XX New isolated Helicobacter polynucleotides - used to develop products
PT for the diagnosis, prevention and treatment of Helicobacter
PT infections and gastrointestinal diseases
XX
XX Claim 8; Page 748-751; 2054pp; English.
XX
XX This sequence represents a Helicobacter pylori GHPO protein of the
CC invention. The polypeptides can be used for preventing or treating
CC Helicobacter infections, and gastroduodenal diseases associated with
CC these infections, including acute, chronic, and atrophic gastritis, and
CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
CC used for the production of antibodies. The products can also be used for
CC detection and diagnosis.
XX
XX Sequence 491 AA;

Query Match 35.8%; Score 996; DB 19; Length 491;
Best Local Similarity 42.9%; Pred. No. 1.4e-90;
Matches 219; Conservative 94; Mismatches 170; Indels 28; Gaps 12;

QY 9 QKVCIVVDGCLSDQHGNAIAKAKTPIMDKLCSG-NWOKLEAHGLHVLGPEGLMGNSE 67
DB 3 QKTLIIITDGIKGRKSDHNAFFHAKKPTDYLMTFLPYSLLDTHGLSVGLPRKQMGNSE 62
QY 68 VGHNLNIGAGRVYQDVRINLAVORNEFTNPQIVASAEKKGSRHLHLGLVSDGGVH 127
DB 63 VGHNLNIGAGRVYQDVRINLAVORNEFTNPQIVASAEKKGSRHLHLGLVSDGGVH 118
QY 128 SHIDHLFALIRAFKQLOPKVPIHFADGRDTSPTSGAGYLEQLQFIASEKYELATIT 187
DB 119 SHIEFIALALECEKSH-KKVCILHITDGRDVAKSAITYLKQ-MONICNESI-QIATIS 175
QY 188 GRVYAMDGRKWERIKMAYEAIVGIGOKATVDKAVDVVRERYAQSEDFELKPIVFSDD 247
DB 176 GRVYAMDGRKWERIKMAYEAIVGIGOKATVDKAVDVVRERYAQSEDFELKPIVFSDD 232
QY 248 GRVYAMDGRKWERIKMAYEAIVGIGOKATVDKAVDVVRERYAQSEDFELKPIVFSDD 307
DB 233 CGMQDDSEFIFINFRNDREAREIVSALQKQFSGFRQV--FKLHIAHTPTDNTFFPV 290
QY 308 LFPVPTHTNVLAEWLASQGVTFQHCATEKYPHVTFFNGREVFQDERCMVSPKEV 367

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291 LFPRESYNTLAEEVVSQHNTQSHIAETEKYAHVTFPINGVETPFKNENRVLIQSPK-V 349
368 ATYDLKPEMAAGVAEKWQIESGRHPLVMCFAPDPMDVGHGTHCKFFPAVKACQATDEAI 427
350 TTYDLKPEMSAKEVTLAVLBQMKLGT-DLIIVNFANGDMVGHGTHGFNFEASVKAVEADACL 408
428 GKIPFACQTYNYLMVTSDHGNAEKMIAPDGESEHTAHTCNLPPTCSKTFVFKSTPPTG 487
409 GEILSLAKKLDYAMLLTSDHCNCERMDENQNPILTNTAG-----SVYCFVL-----G 456
488 DDGKE-RARALRDVAPTVLQMLGLPVPPEMD 517
457 DGVKSIRKNGALNNIASSVLMGLKAPATMD 487

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RESULT 3

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AAG82563
ID AAG82563 standard; Protein; 505 AA.
XX
AC AAG82563;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis open reading frame protein sequence SEQ ID NO:2220.
XX
KW Staphylococcus epidermidis SR1 strain; infection; diagnosis;
KW vaccination; endocarditis.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000MO-US30782.
XX
PR 09-NOV-1999; 99US-0164258.
XX
PA (GLAXO ) GLAXO GROUP LTD.
XX
PI Kimmerly WJ;
XX
DR WPI; 2001-316495/33.
XX
DR N-PSDB; AAH53413.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis -
XX
PS Claim 18; Page 595; 2188pp; English.
XX

```

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the amplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though the sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.

Sequence 505 AA;

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Query Match 35.6%; Score 992; DB 22; Length 505;
Best Local Similarity 39.2%; Pred. No. 3.6e-90;
Matches 205; Conservative 94; Mismatches 196; Indels 28; Gaps 8;
QY 8 QQKVCYLVIDGWSLDSQHGNAIAKAKTIPIMDKLCSGNWQK-----LEAHGLHVLGPEGL 62
DB 3 KQPTALLIDGFANRESEHGNAVKQAHKPNFDY---YKYPPTQTIEASGLDVLGPEGG 58
QY 63 MGNSEVGHNTGAGRVIIYQDIVRLINLAVQRNEFTNPQIVASAEARAKKSGRLHLGLVS 122
DB 59 MGNSEVGHMIGAGRIYVQSLTRINKSIEDGEFDNTVLNNNAVHVKDNGSALHVFGLLS 118
QY 123 DGGVSHIDHLFALIRAFKQLOQVPKVFTHFFADRGDTSPTSAGYLEQLLOQFIASEKYGE 182
DB 119 DGGVSHYKHLFAILELAKKQIDKVVYVHAFLDRDVRDOKSALKYIEETEDKFKELGVGQ 178
QY 183 LATITGRYAMDRDKRWERIKMAYEIAIVGGIGQATVDKAVDVVVRERYAQSETEFLKPI 242
DB 179 FASVSGRYAMDRDKRWDRERAYNAIRNFEPTTSAKA--GVEANYKNDVTDFEVEPF 236
QY 243 VF--SDDGRYKDDDTLIFFFNYRADMRQICECLGLERYKDLNSSVPHPKNIQISGMYQN 300
DB 237 IVEQNDG-VNDGDAVIFYNRPDRAAQLSEIFTNKAFDGF--KVEQVDNLFYATFTKYN 293
QY 301 KERPPEPSPVPTHTNVLAEWLASQVYTFQPHCAETEKYPHYVTFEFGNGREYQFODEECM 360
DB 294 DNVDAEIVFEKVDLNNITGEVAQDNGLKQLRIATEKYPHYTFMWSGRNEEFEGERRRL 353
QY 361 VPSPKEVATYDLKPEMNAAGVAEKWQIESGRHPLVMCFAPDPMDVGHGTHCKFFPAVKAC 420
DB 354 IDSPK-VATYDLKPEMSAYEVKDALLELDKGLDILLNFANPDMVGHSGMLEPTIKAI 412
QY 421 QATDEATGKFEACQTYNYLMVTSDHGNAEKMIAPDGESEHTAHTCNLPPTCSKTFV 480
DB 413 EAVDECLGEVYVDKIIDMGHAIITADHNSQVLTDDDDQPMTHHTNPVPVITKEGVT 472
QY 481 KSTPPTGDDGKERARALRDVAPTVLQMLGLPVPPEMDGVPLLE 523
DB 473 RETGRLG-----DLAPTLLDLLNVKQPMSEMTGESLIK 504

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RESULT 4

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ABP40599
ID ABP40599 standard; Protein; 517 AA.
XX
AC ABP40599;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5444.
XX
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy.
XX
OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-0134001.
XX
PR 14-AUG-1997; 97US-055779P.
XX
PR 08-NOV-1997; 97US-064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
XX WPI; 2002-381255/41.
XX
XX N-PSDB; AEN93144.
XX

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```
Db      422 VRVNIPNGDMVGHRTGDEATVVACKAADEAVKMILDAVEQVGGIYVVTADHGNADMVKR 481
OY      455 -----APDSEH--TAHTCNLYPFTCS-----SKTFVFKSTPTTGGDKERARALRDVA 501
Db      482 NKGEPILKDEVOILVSHTLQPVPIAIGGFLSAGVRFKRDVPSPG-----GLANVA 533
OY      502 PTVLQLMGLPVPPEMD 517
Db      534 ATVMNLHGFVAPEDYE 549

RESULT 6
AAG38644
ID      AAG38644 standard; Protein; 560 AA.
AC      AAG38644;
XX
XX      DT      18-OCT-2000 (first entry)
XX
XX      DE      Arabidopsis thaliana protein fragment SEQ ID NO: 47704.
XX
XX      KW      Protein identification; signal transduction pathway; metabolic pathway;
KW      hybridisation assay; genetic mapping; gene expression control; promoter;
KW      termination sequence.
XX
XX      OS      Arabidopsis thaliana.
XX
XX      PN      EP1033405-A2.
XX
XX      PD      06-SEP-2000.
XX
XX      PF      25-FEB-2000; 2000EP-0301439.
XX
XX      PR      25-FEB-1999; 99US-0121825.
XX      PR      05-MAR-1999; 99US-0123180.
XX      PR      09-MAR-1999; 99US-0123548.
XX      PR      23-MAR-1999; 99US-0125788.
XX      PR      25-MAR-1999; 99US-0126264.
XX      PR      29-MAR-1999; 99US-0126785.
XX      PR      01-APR-1999; 99US-0127462.
XX      PR      06-APR-1999; 99US-0128234.
XX      PR      08-APR-1999; 99US-0128714.
XX      PR      16-APR-1999; 99US-0129845.
XX      PR      19-APR-1999; 99US-0130077.
XX      PR      21-APR-1999; 99US-0130449.
XX      PR      23-APR-1999; 99US-0130510.
XX      PR      28-APR-1999; 99US-0130891.
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XX      PR      04-MAY-1999; 99US-0132407.
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XX      PR      06-MAY-1999; 99US-0132486.
XX      PR      07-MAY-1999; 99US-0132487.
XX      PR      11-MAY-1999; 99US-0132863.
XX      PR      14-MAY-1999; 99US-0134256.
XX      PR      14-MAY-1999; 99US-0134218.
XX      PR      14-MAY-1999; 99US-0134219.
XX      PR      14-MAY-1999; 99US-0134221.
XX      PR      14-MAY-1999; 99US-0134370.
XX      PR      18-MAY-1999; 99US-0134768.
XX      PR      19-MAY-1999; 99US-0134941.
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XX      PR      21-MAY-1999; 99US-0135353.
XX      PR      24-MAY-1999; 99US-0135629.
XX      PR      25-MAY-1999; 99US-0136021.
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XX      PR      01-JUL-1999; 99US-0141842.
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XX      PR      02-JUL-1999; 99US-0142055.
XX      PR      06-JUL-1999; 99US-0142390.
XX      PR      08-JUL-1999; 99US-0142803.
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XX      PR      12-JUL-1999; 99US-0142977.
XX      PR      13-JUL-1999; 99US-0143542.
XX      PR      14-JUL-1999; 99US-0143624.
XX      PR      15-JUL-1999; 99US-0144005.
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 Best Local Similarity 34.9%; Pred. No. 1e-63;
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QY	129	HIDHLFALIRAFKQLQVPRVFIHFFADGRDTSPTSGAGVLEQLLQFIASEKY----GELA 184
Db	143	RLDQVOLLKGAERGAARIRVHILTDGRDVLDSGSGVGFETLEADLAALRAKGVDAQVA 202
QY	185	TITGR-YYAMDR-DKWERIKMAYEA-IVGGIGQKATVDKAVDVWRERVAQ-SETDEFK 240
Db	203	SGGGRMYVTMDRYENDWSVVKGWDQAQVLGEAPHK--FKSALEAVKTLRAEPCANDQYLP 260
QY	241	PIVFSDD-----GRVKDDDTLFFNYRADRMQICECLGLERYKDLNS----SVPHPKNI 291
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Db	433	VGHTGDIEATVAVACEAADRAVRTILDAIEOVGGIYVVTADHGNADVMVRDKSGKPALDK 492
QY	462	-----TAHTCNLPFTCS---SKTFVFK---STPPTGDDGKERARALRDVAPTVQL 507
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RESULT 7
 AAG26479
 ID AAG26479 standard; Protein; 557 AA.
 AC AAG26479;
 XX AAG26479;
 DT 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 30950.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 PN EP1033405-A2;
 XX EP1033405-A2;
 PD 06-SEP-2000.
 XX 06-SEP-2000.
 PF 25-FEB-2000; 2000EP-0301439.
 XX 25-FEB-1999; 99US-0121825.
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QY 513 PPEND 517
Db 548 PDDYE 552

RESULT 9
AAW28502
ID AAW28502 standard; Protein; 556 AA.
XX AAW28502;
DT 07-JAN-1998 (first entry)
XX Timothy grass pollen co-factor-independent phosphoglycerate mutase
DE Isoform Phl1.
XX Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW Timothy grass; pollen; allergy; plant allergen; panallergen; B cell;
KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
XX conserved.
OS Phleum pratense L.
XX W09705258-A2.
XX 13-FEB-1997.
XX 02-AUG-1996; 96WO-AT00141.
XX 02-AUG-1995; 95AT-0001320.
XX (BIOM-) BIOMAY PROD N & HANDELS GMBH.
XX Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
PI Kraft D, Richter K, Rheinberger H;
XX WPI: 1997-145695/13.
XX N-PSDB; AAT86243.
PT New recombinant DNA encoding plant phosphoglycerate mutase or its
PT antigenic epitope(s) - useful for diagnosis or treatment of
PT allergies to pollen and plant-derived foods
XX Claim 1; Fig 7a; 160pp; German.
XX AAW28502 shows Timothy grass pollen co-factor-independent
CC phosphoglycerate mutase (PGM-i) isoform Phl1. PGM-i is a highly conserved
CC plant allergen (panallergen) which can cause cross-reactivity in patients
CC allergic to pollen and plant-derived foods. PGM-i and it's B cell and T
CC cell epitopes can be used for the in vitro detection of allergy against
CC PGM-i, by measuring serum IgE or a cellular reaction. They can also be
CC used in immunotherapy and will not cause an autoimmune response because
CC PGM-i is significantly different from the human enzyme, which is
CC co-factor dependent.
XX
SQ Sequence 556 AA;

Query Match 25.0%; Score 696; DB 18; Length 556;

Best Local Similarity 33.9%; Pred. No. 2.le-60;
Matches 186; Conservative 92; Mismatches 210; Indels 60; Gaps 21;
QY 11 VCLVIVDGLSDEQHGNAITAKAKTPTMDKLCSG---NWQKLEAHGLHVCLP-EGLMGNS 66
Db 19 VAVIVLDGNGEASADQYNCIHRAETPYMDSLKNGAPEKWTLVKAHTGAVGLPDDDDMGNS 78
QY 67 EVGHLNIGAGRVTYQDIVRINLAVORNEFTNPQIVASAEAKKSGRLLHLLGLVSDGGV 126
Db 79 EVGHNALGAGRIFAQGAOKLFDAAASGKIWEDSGFNKESPAEET--LHLIGLLSDGGV 136
QY 127 HSHIDLHALIRAFKQLQVPKVFIFHFADGRDTSPTSGAGYLBOLLOQFIAS--EK---YGE 182
Db 137 HSLRDQVQLLVKVASERGAKRIRLHILTDGRDLVLDGSSGVFVETLENDLAQLREKGVDAQ 196
QY 183 LATITGR--YYAMDR-DKRWERIKMAYEA--IVGGIGOKATVDKAVDVVRERYAQSE--TDEF 238
Db 197 VASGGGRMYVTMDRYENDWDVVRGMDAQVIGEPYK--FKSALEAVKTLRAEPKANDQY 254
QY 239 LKPIVFSDD-----GRVKDDDTLIFFNVRADMRQICEGLERYKDLNSVPHPKNIQI 293
Db 255 LPAFVIVDESGKSVGPVVDGDAVVIFNFRADRVMLAKALEFADE--DKEDRVVPK-IKY 312
QY 294 SGMTOYNKEPFPPLF---PPVTHTNVLAEMLASQGVTFQHCATEKYPHVTFEFGNGRE 350
Db 313 AGMLQYDGLKLPKFLVSPPLIE-RTSGEYLVNNGVTRTFACSETVKFGHVTFFWNGNRS 371
QY 351 VQFQD--EERCMPSPKEVATYDLKPEMNAAGVAEKWVEIESGRHPLVMCNFAPDMVG 408
Db 372 GFDETKEEYIEIPSDSGI-TFNEQPKMALEIAEKTRDAILSKFOVRLNPNMGDMVG 430
QY 409 HTGKFEPAVKACATDAIGKIFACOTYNNVLMVTSDHGNAEKMIAPDGSEH----- 461
Db 431 HTGDIATVTVACKAADAVAKMILDAIKVEGGIYVTVADHGNADVMYRNKSGQALDKSG 490
QY 462 -----TAHTCNLPVFTCSKTF-----VFKS---TPPTGDDGKERARALRDVAPTVLQMLG 509
Db 491 SIQILTSHTLQPVPAIGGPGLPGLHPGVKFRSDINTP-----GLANVAATVMNLHG 539
QY 510 LPVPPEND 517
Db 540 FOAPDDYE 547

RESULT 10
AAW28503
ID AAW28503 standard; Protein; 555 AA.
XX AAW28503;
DT 07-JAN-1998 (first entry)
XX Timothy grass pollen co-factor-independent phosphoglycerate mutase
DE Isoform Phl5.
XX Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW Timothy grass; pollen; allergy; plant allergen; panallergen; B cell;
KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
XX conserved.
OS Phleum pratense L.
XX W09705258-A2.
XX 13-FEB-1997.
XX 02-AUG-1996; 96WO-AT00141.
XX 02-AUG-1995; 95AT-0001320.
XX (BIOM-) BIOMAY PROD N & HANDELS GMBH.
XX Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
PI Kraft D, Richter K, Rheinberger H;

PR	18-JUN-1999;	99US-01397750.	PR	27-AUG-1999;	99US-0151065.
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PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
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PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
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PR	29-OCT-1999;	99US-0162142.	PR	29-OCT-1999;	99US-0162142.
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Query Match			24.7%; Score 687; DB 21; Length 575;		
Best Local Similarity			33.3%; Pred. No. 1.8e-59;		
Matches 189; Conservative			85; Mismatches 213; Indels 80; Gaps 22;		
Qy	11	VCLVVDGWSLDEQHGNAIAKAKTPIMDKLCSG---NWQKLEAHGLHWGLP-EGLMGNS 66			
Db	21	IATIVLDGWGESAPDQYNCIHNAPTAMDLSKHGAPDTWTLLKHAHTAVGLPSEDDMGNS 80			
Qy	67	EVGHNLITAGRVIIYODIVRINLAVORNEFVTNPQIVASAEAKKSGRLHLGLVSDGV 126			
Db	81	EVGHNLGAGRIFAQGAQKALCDQALASGKIFEGEGFKYVSSEFE--TNTLHLVGLSDGV 138			
Qy	127	HSIDHLEFALLIRAFKQLQVPKVFTHFFADGDRDTSTSGAGLYEQL-LQFIASEKYG---E 182			
Db	139	HSRLDQLQLLIKSAERGAIRVHILTDGRDVLGSSVGFVETLEADLVALRENGVDAQ 198			
Qy	183	LATITGR--YAMDR-DKRWERIKMAYEA-IVGGIGQKATVDKAVDVVRE-RYAQSETDEF 238			
Db	199	IASGGGRMYVTILDREYNDWEVVKRGWDAQVILGEAPHK--FKNVAEAVTLKKEPGANDQY 256			
Qy	239	LKPIVFSDD-----GRVKDDDTLIFPNYRADRMROIQCEGLERYKDLNLSVPHPKNIQI 293			

Db 257 LPPEFVDSGKAVGPIVDGDAVVTENFRADRMVMAKALEYEDF-DKFDVRYPK-IRY 314
QY 294 SGWTOYNKEFPFSLF-----PPVTHNVLAEWLASOGVTFQFCA----- 333
Db 315 AGMLQYDGLKLPRLSVLPPEIDRTS--GEYLTHNGVSTFACSSCLLIIGLYALHFC 372
QY 334 --ETERYPHVTFPFGNGREVQFOD--EERCWVSPKEVATYDLKPMNAAGVAEKVQEI 389
Db 373 QYETVFGHVTFFWNGNRSGYFNEKLEEVPEIPSDSGI--SFNVQPKMALEIGEKAARDAI 431
QY 390 ESCRHPLVMCNFAPPDMVGHGTFKPEPAVKACQATDEAIGKIFACQTYNYVLMVTSDHGN 449
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QY 450 AEKMIAPDGEH-----TAHTCNLYPFTCSSTFV-----FK-----STPPTGDDG 490
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QY 491 KERARALRDVAPTVLQMLGLPVPPEMD 517
Db 546 -----GLANVAATVMNLHGFAVPSDYE 567

RESULT 12

AAW28501
ID AAW28501 standard; Protein; 530 AA.

XX AC AAW28501;

XX DT 07-JAN-1998 (first entry)

XX DE Birch pollen co-factor-Independent phosphoglycerate mutase.

XX KW Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.21;
KW birch; pollen; allergen; plant allergen; panallergen; B cell;
KW t cell; epitope; immunotherapy; detection; diagnosis; hay fever;
XX conserved.

XX OS Betula verrucosa.

XX PN WO9705258-A2.

XX PD 13-FEB-1997.

XX PF 02-AUG-1996; 96WO-AT00141.

XX PR 02-AUG-1995; 95AT-0001320.

XX PA (BIOM-) BIOMAY PRODN & HANDELS GMBH.

XX PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
PI Kraft D, Richter K, Rheinberger H;

XX XX WPI; 1997-145695/13.

XX DR N-PSDB; AAT86242.

XX PT New recombinant DNA encoding plant phosphoglycerate mutase or its
PT antigenic epitope(s) - useful for diagnosis or treatment of
PT allergies to pollen and plant-derived foods

XX PS Claim 1; Fig 1; 160pp; German.

XX CC AAW28501 is a birch pollen co-factor-independent phosphoglycerate
CC mutase (PGM-i). PGM-i is a highly conserved plant allergen (panallergen)
CC which can cause cross-reactivity in patients allergic to pollen and
CC plant-derived foods. PGM-i and its B cell and T cell epitopes can be
CC used for the in vitro detection of allergy against PGM-i, by measuring
CC serum IgE or a cellular reaction. They can also be used in immunotherapy
CC and will not cause an autoimmune response because PGM-i is significantly
CC different from the human enzyme, which is co-factor dependent.

XX SQ Sequence 530 AA;

Query Match 24.6%; Score 686; DB 18; Length 530;
Best Local Similarity 36.0%; Pred. No. 1.9e-59;
Matches 191; Conservative 73; Mismatches 208; Indels 58; Gaps 20;
QY 28 NAIKAKTPTMDKLCSG---NMQKLEAHLGLVGLP-EGLMGNSEVGHLMIGRVIYQDI 83
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QY 84 VRINLAVQRNEFVNPQIVASAEKAKGSGRLHLGLVSDGGVHSHIDHFLALIRAFKQL 143
Db 70 KLVDLSALASGKIYEGEGFYIKCECFENG--LHLIGLSDGGVHSHLDQLLLKGAER 127
QY 144 QVPKVFIFHFADRGRTSPTSGAGYLRQLLOFTAS--EK--YGLATITGR--YYAMDR-DK 197
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QY 250 VKDDDTLIFFNVRADRMROIICELGLERYKDLNSSVPHPKNIOISGMTQYNKEFPFSLF 309
Db 245 IVDGDVAVTINFRADRMVMAKALEYENF-DKIDRVRFK-IRYAGMLQYDGLKLPVSHY 302
QY 310 ----PPVTHNVLAEWLASOGVTFQFCAETERYPHVTFPFGNGREVQFOD--EERCWVSP 363
Db 303 LVEPPEIERTS--GEYLHNGVTFACSETVRFVGHVTFWNGNRSGYFNESELEYVEIPS 360
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QY 472 TCSSKTFV----FKSTPPTGDDGKERARALRDVAPTVLQMLGLPVPPEMD 517
Db 480 AIGGPALASGVRFCDLDPG-----GLANVAATVMNLHGFEAPSDYE 521

RESULT 13

AAW38645
ID AAW38645 standard; Protein; 511 AA.

XX AC AAW38645;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 47705.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 25-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

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XX PR 08-APR-1999; 99US-0128714.

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Query Match 23.2%; Score 647; DB 21; Length 510;

Best Local Similarity 34.1%; Pred. No. 1.5e-55;
Matches 178; Conservative 81; Mismatches 201; Indels 62; Gaps 21;
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QY 94 EFTVNPQIVASAEKAKKSGRLHLGLVSDGGVHSHDLHLFALIRAFKQLQVQKVFHFHF 153
Db 61 KIFEGEGFKYVSESFE--TNTLHLVGLSDGGVHSHDLQLLLIKSAERKAKRIRVHIL 118
QY 154 ADGRDTSPTSGAGYLEOL-LQFTASEKYG---ELATTIGR-YAMDR-DKRWERIKWAYE 207
Db 119 TQGRDVLDSGSGVGFVETLEADLVALRENGVDAQIASGSGRMVYVTLDRYENDWEYVKKRGWD 178
QY 208 A-IVGGIGQKATVDKAVDVVRE-RYAOSETDEFKLPVFSDD-----GRVKDDDTLIFEN 260
Db 179 AQVLGEAPHK--FKNAVEAVKTLRKEPGANDQYLPFPFVVDSEKAVGPIVDGAVVTEN 236
QY 261 YRADRMQICEICGLERYKDLNSSVPHPKNTIQISGMTQYNKEFPFPLF-----PPVTHTN 316

Db 237 FRADRMVMAKALEYEDF-DKFDVRYPK-IRYAGMLQYDGLKLPRLVSPPEIDRTS 294
QY 317 VLAELASOGVTFQHCATEKYPHVTFFENGREVOFQD--EERCMPVSPKEVATYDLAP 374
Db 295 --GEYTHGVSTFACSEYVKGHVTFFWNGNRSGYFNKLEBYVIPSDSGI-SFNVOP 351
QY 375 EMNAAGVAEKVMEQIESGRHPLVMCFAPPPDMVGHGTPKPEPAVKACQATDEAIGKIFEAC 434
Db 352 KMKALEIGEKARDAILSGKFDQVRVNI PNGDMVGHGTDIEATVFACEAADLAVKMFDAI 411
QY 435 QYNYNYLMTSDHGNAEKMIADPGSEH-----TAHTCNLVPTCSKSTV--- 479
Db 412 EQVKGIYVTVADHGNADVKRDKSGKPAIDKEGKLIQILTSHTLKEVPPIAGGPGLAQGV 471
QY 480 -FK---STPPTGDDGRERARLRDVAPTVLQMLGPPVPEMD 517
Db 472 RFRKDLTP-----GLANVAATVYNLHGFVAPSDYE 502

RESULT 15
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XX AC AAG30863;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 36972.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
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Best Local Similarity 33.08; Pred. No. 1.3e-53;
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Qy 208 A-IVGGIGQKATVDKAVDVVRE-RYAOSETDEFKPIVFSDD----GRVKDDDTLIFFN 260
Db 179 AOVLEAPHK--FKNAVEAVKTLRKEPCANDQYLPFPFVIVDESGKAVGPVVDGDAVTFN 236
Qy 261 YRADMRQICBCLGLERYKDLNSSVPHPKNTQISGMTQYKKEFPFPSLF-----PPVHTN 316
Db 237 FRADRMVMAKALEYEDF-DKFDVRYPK-IRYAGMLQYDGLKLPSPRYLSPPEIDRTS 294
Qy 317 VLAEWLASQGVTOFHCA-----ETEKYPHTVTFEFGGREGVOFQD--E 356
Db 295 --GEYLTHNGVSTFACSSCLLIIGLYALHFCQYETVKFGHVTFFWNGNRSGYFNEKLE 352
Qy 357 ERCMVPSPKEVATYDLKPEMNAAGVAENKVNQIESGRHPLVMCNFAPDPMDVGHGKFERPA 416
Db 353 EYVEIPSDSGI-SFNVPQKKALEIGEKAIDAILSGKFDQVRVNIPLNGDMVGHGTDIEAT 411
Qy 417 VKACQATDEAIGKIFACQTYNYVLMVTSDHGNAEKMIAPGSEH-----TAH 464
Db 412 WVACEAADLAVKMIFDAIEQVKGIYVVVTADHGNADVMVKRDKSGKPAIDKEGKLQILTSH 471
Qy 465 TCNLVPFTCSSKTFV---FK---STPPTGDDGKERARALRDVAPTVLQMLPVPPEMD 517
Db 472 TLKPVPPIAIGGPGLAQGVRFRRKDLTP-----GLANVAATVMNLHGFVAPSDYE 520

Search completed: July 31, 2003, 13:32:23
Job time : 86 secs

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